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RAW SEQUENCE LISTING

DATE: 12/26/2002

PATENT APPLICATION: US/09/936,883C

TIME: 13:07:26

Input Set : D:\Seqlist.txt

Output Set: N:\CRF4\12262002\I936883C.raw

3 <110> APPLICANT: MIYATA, Toshio
5 <120> TITLE OF INVENTION: A Method for Detecting Megsin Protein and Use
6 Thereof
8 <130> FILE REFERENCE: F2-101DP1PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/936,883C
C--> 11 <141> CURRENT FILING DATE: 2001-12-21
13 <150> PRIOR APPLICATION NUMBER: JP 1999-75305
14 <151> PRIOR FILING DATE: 1999-03-19
16 <150> PRIOR APPLICATION NUMBER: JP 1999-306623
17 <151> PRIOR FILING DATE: 1999-10-28
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1143
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1140)
32 <300> PUBLICATION INFORMATION:
33 <302> TITLE: A mesangium-predominant gene, megsin, is a new serpin
34 upregulated in IgA nephropathy.
35 <303> JOURNAL: J. Clin. Invest.
36 <304> VOLUME: 120
37 <305> ISSUE: 4
38 <306> PAGES: 828-836
39 <307> DATE: 1998-08-15
41 <400> SEQUENCE: 1
42 atg gcc tcc ctt gct gca gca aat gca gag ttt tgc ttc aac ctg ttc 48
43 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe
44 1 5 10 15
46 aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct 96
47 Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
48 20 25 30
50 ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat 144
51 Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
52 35 40 45
54 gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca 192
55 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
56 50 55 60
58 gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg 240
59 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
60 65 70 75 80

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62 aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc 288
63 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
64      85      90      95
66 agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag 336
67 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
68      100      105      110
70 gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga 384
71 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
72      115      120      125
74 gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag 432
75 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys
76      130      135      140
78 tgg gtt gaa aat gaa aca cat ggc aaa atc aag aac gtg att ggt gaa 480
79 Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
80 145      150      155      160
82 ggt ggc ata agc tca tct gct gta atg gtg ctg gtg aat gct gtg tac 528
83 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
84      165      170      175
86 ttc aaa ggc aag tgg caa tca gcc ttc acc aag agc gaa acc ata aat 576
87 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
88      180      185      190
90 tgc cat ttc aaa tct ccc aag tgc tct ggg aag gca gtc gcc atg atg 624
91 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
92      195      200      205
94 cat cag gaa cgg aag ttc aat ttg tct gtt att gag gac cca tca atg 672
95 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
96      210      215      220
98 aag att ctt gag ctc aga tac aat ggt ggc ata aac atg tac gtt ctg 720
99 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
100 225      230      235      240
102 ctg cct gag aat gac ctc tct gaa att gaa aac aaa ctg acc ttt cag 768
103 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
104      245      250      255
106 aat cta atg gaa tgg acc aat cca agg cga atg acc tct aag tat gtt 816
107 Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
108      260      265      270
110 gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa 864
111 Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
112      275      280      285
114 caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa 912
115 Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
116      290      295      300
118 gca gat ctc tct ggg att gct tcg ggg ggt cgt ctg tat ata tca agg 960
119 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
120 305      310      315      320
122 atg atg cac aaa tct tac ata gag gtc act gag gag ggc acc gag gct 1008
123 Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
124      325      330      335
126 act gct gcc aca gga agt aat att gta gaa aag caa ctc cct cag tcc 1056

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127 Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
128          340          345          350
130 acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat 1104
131 Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
132          355          360          365
134 gac atc atc tta ttc agt ggc aaa gtt tct tgc cct tga 1143
135 Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro
136          370          375          380
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 380
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
145 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe
146   1          5          10          15
148 Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
149          20          25          30
151 Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
152          35          40          45
154 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
155          50          55          60
157 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
158   65          70          75          80
160 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
161          85          90          95
163 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
164          100          105          110
166 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
167          115          120          125
169 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys
170          130          135          140
172 Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
173 145          150          155          160
175 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
176          165          170          175
178 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
179          180          185          190
181 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
182          195          200          205
184 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
185          210          215          220
187 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
188 225          230          235          240
190 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
191          245          250          255
193 Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
194          260          265          270
196 Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
197          275          280          285

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```

199 Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
200      290                      295                      300
202 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
203 305                      310                      315                      320
205 Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
206                      325                      330                      335
208 Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
209                      340                      345                      350
211 Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
212                      355                      360                      365
214 Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro
215      370                      375                      380
218 <210> SEQ ID NO: 3
219 <211> LENGTH: 29
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
225      synthesized degenerative primer sequence
227 <220> FEATURE:
228 <221> NAME/KEY: misc_feature
229 <222> LOCATION: 26, 29
230 <223> OTHER INFORMATION: n is a or g or c or t.
232 <400> SEQUENCE: 3
W--> 233 gtgaatgctg tgtacttaaa ggcaantgn 29
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 17
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
243      synthesized degenerative primer sequence
245 <220> FEATURE:
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: 3, 9, 15
248 <223> OTHER INFORMATION: n is a or g or c or t.
250 <400> SEQUENCE: 4
W--> 251 aanagraang grtcngc 17
254 <210> SEQ ID NO: 5
255 <211> LENGTH: 26
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
261      synthesized degenerative primer sequence
263 <220> FEATURE:
264 <221> NAME/KEY: misc_feature
265 <222> LOCATION: 6, 9, 12, 15, 18, 21
266 <223> OTHER INFORMATION: n is a or g or c or t.

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268 <400> SEQUENCE: 5
W--> 269 atggcntcng cngcngcngc naaygc 26
272 <210> SEQ ID NO: 6
273 <211> LENGTH: 37
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
279 synthesized degenerative primer sequence
281 <400> SEQUENCE: 6
282 cgacctccag aggcaattcc agagagatca gccctgg 37
285 <210> SEQ ID NO: 7
286 <211> LENGTH: 34
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
292 synthesized degenerative primer sequence
294 <400> SEQUENCE: 7
295 gtcttccaag cctacagatt tcaagtggct cctc 34
298 <210> SEQ ID NO: 8
299 <211> LENGTH: 30
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
305 synthesized antisense primer sequence
307 <400> SEQUENCE: 8
308 gctcagggca gtgaagatgc tcagggaaga 30
311 <210> SEQ ID NO: 9
312 <211> LENGTH: 27
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
318 synthesized antisense primer sequence
320 <400> SEQUENCE: 9
321 ctgacgtgca cagtcacctc gagcacc 27
324 <210> SEQ ID NO: 10
325 <211> LENGTH: 36
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
331 synthesized sense primer sequence
333 <400> SEQUENCE: 10
334 gaggtctcag aagaaggcac tgaggcaact gctgcc 36
337 <210> SEQ ID NO: 11
338 <211> LENGTH: 15

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 26, 29
Seq#:4; N Pos. 3, 9, 15
Seq#:5; N Pos. 6, 9, 12, 15, 18, 21
Seq#:18; N Pos. 158, 159, 160, 287, 288, 289
Seq#:18; Xaa Pos. 51, 94
Seq#:19; Xaa Pos. 51, 94